



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2000, 08:09:53 ; Search time 1236.72 Seconds  
(without alignments)  
-502.631 Million cell updates/sec

Title: PCT-US00-04950-1-COPY\_4912\_5550  
Sequence: 1 gaggtgacgcacagcctag.....tggagcgcagcctccccc 639

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 882769 seqs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database:

- 1: gb\_ba1.\*
- 2: gb\_ba2.\*
- 3: gb\_om.\*
- 4: gb\_om.\*
- 5: gb\_pat.\*
- 6: gb\_ph.\*
- 7: gb\_ph.\*
- 8: gb\_ph.\*
- 9: gb\_ph.\*
- 10: gb\_ph.\*
- 11: gb\_ph.\*
- 12: gb\_ph.\*
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- 39: gb\_ph.\*
- 40: gb\_ph.\*
- 41: gb\_ph.\*
- 42: gb\_ph.\*
- 43: gb\_ph.\*
- 44: gb\_ph.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	639	100.0	5492	40	AF123659	AF123659 Homo sapi
2	639	100.0	9108	40	AF123653	AF123653 Homo sapi
3	434	67.9	1722	40	AF123658	AF123658 Homo sapi
4	374	58.5	1692	40	AF123657	AF123657 Homo sapi
5	224.4	35.1	1614	40	AF123655	AF123655 Homo sapi
6	175.4	27.4	1515	40	AF123656	AF123656 Homo sapi
7	148.2	23.2	188817	33	AL13315	AL13315 Homo sapi
8	125.2	19.6	5257	9	AB011124	AB011124 Homo sapi
9	125.2	19.6	159898	33	HS1187M17	HS1187M17 Homo sapi
10	114.4	17.9	3452	14	U02454	U02454 Cloning vec
11	114.4	17.9	9600	5	A92865	A92865 Sequence 1
12	114.4	17.9	10596	5	I25041	I25041 Sequence 15
13	114.4	17.9	10596	5	I30503	I30503 Sequence 15
14	114.4	17.9	10596	5	XX002428	XX002428 Cloning vec
15	114.4	17.9	10737	14	U02455	U02455 Cloning vec
16	114.4	17.9	10850	14	U02455	U02455 Epstein-Bar
17	114.4	17.9	172281	16	EBV	EBV Epstein-Bar
18	114.4	17.9	184113	16	HS4B958RAJ	HS4B958RAJ Mus muscu
19	104.4	15.6	5719	12	MCATSI	MCATSI Mus muscu
20	99.4	15.6	97348	12	AF091216	AF091216 Mus muscu
21	97.6	15.3	166171	42	AC011767	AC011767 Homo sapi
22	95.8	15.0	2508	9	ORAINVOL	ORAINVOL Homo sapi
23	94.6	14.8	59686	42	AC016204	AC016204 Homo sapi
24	93.2	14.6	460	12	MUSIR3E1	MUSIR3E1 Homo sapi
25	88.8	13.9	3489	16	KS052064	KS052064 Homo sapi
26	88.8	13.9	32207	5	AR065852	AR065852 Sequence
27	88.8	13.9	137508	16	KS075658	KS075658 Sequence
28	88.8	13.9	2793	5	AR009990	AR009990 Sequence
29	88.6	13.9	2793	5	I95876	I95876 Sequence 1
30	88.6	13.9	3060	35	AF027735	AF027735 Nephila c
31	86.6	13.6	5721	9	AB002339	AB002339 Human MRN
32	86.2	13.5	28559	16	AF148805	AF148805 Kaposi's sa
33	84.8	13.3	1369	9	GIBINVOL	GIBINVOL Kaposi's sa
34	84.6	13.2	46288	4	FR090880	FR090880 Pugu rubrid
35	84.6	13.1	3941	12	RNLAR2	RNLAR2 R. norvegicu
36	83.6	13.1	2479	12	RN087960	RN087960 Rattus norv
37	83.2	13.0	451	12	MUSIR3E2	MUSIR3E2 Mus muscu
38	83.2	13.0	1683	9	CHIRIVOL	CHIRIVOL Mus muscu
39	83.2	13.0	1908	5	GORIVOLUA	GORIVOLUA Gorilla gor
40	83.2	13.0	2000	9	PFACSG	PFACSG P. cynomolg
41	83.2	12.9	1281	34	M23604	M23604 Gorilla gor
42	82.2	12.9	1818	16	U93872	U93872 Kaposi's sa
43	81.6	12.8	133661	35	NCU20329	NCU20329 Nephila cla
44	81.2	12.7	1726	12	MUSIR3E3	MUSIR3E3 Mus muscu
45	80.8	12.6	943	12	MUSIR3E3	MUSIR3E3 Mus muscu

ALIGNMENTS

[illegible]

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OM nucleic - nucleic search, using sw model

Run on: June 15, 2000, 02:09:08 ; Search time 1236.72 seconds

(without alignments)  
-271.374 Million cell updates/sec

Title: PCT-US00-04950-1-COPY\_112\_456

Perfect score: 345

Sequence: 1 tcgcagctacagctgcgca.....gcaggagaaagcaaatggg 345

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 882769 segs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

GenEmbl:

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_com:\*  
4: gb\_ov:\*  
5: gb\_pat:\*  
6: gb\_ph:\*  
7: gb\_pi1:\*  
8: gb\_pi2:\*  
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10: gb\_pi4:\*  
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12: gb\_pi6:\*  
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14: gb\_pi8:\*  
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40: gb\_pi34:\*  
41: gb\_pi35:\*  
42: gb\_pi36:\*  
43: gb\_pi37:\*  
44: gb\_pi38:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	345	100.0	9108 40	AF123653 Homo sapi
2	286	82.9	633 40	AF123654 Homo sapi
3	286	82.9	1515 40	AF123655 Homo sapi
4	286	82.9	1614 40	AF123656 Homo sapi
5	286	82.9	1692 40	AF123657 Homo sapi
6	286	82.9	1722 40	AF123658 Homo sapi
7	286	82.9	5492 40	AF123659 Homo sapi
8	106	30.7	231 40	AF123652 Homo sapi
9	39.6	11.5	3496 1	PSEMPA
10	39.6	11.5	3496 5	E03105
11	38.6	11.2	324 5	E15909
12	38.6	11.2	873 1	DVPRCC3
13	36.8	10.7	25970 1	SC2H4
14	36.6	10.6	1884 12	AF050418
15	36.4	10.6	4800 7	M2EMAX
16	36.4	10.6	4800 7	ZMAMAX
17	35.6	10.3	151291 44	AC011772
18	35.2	10.2	2072 12	AF040746
19	35.2	10.2	4501 2	STMXLNA
20	35.2	10.2	35654 1	SC7H1
21	34.8	10.1	1339 8	HVU57845
22	34.8	10.1	29641 35	AC005802
23	34.8	10.1	186298 40	AC007860
24	34.6	10.0	5140 9	AB014541
25	34.6	10.0	190702 44	AC008755
26	34.4	10.0	3831 2	AF159691
27	34	9.9	4788 7	BLYSIPA
28	34	9.9	9830 2	AFACBD
29	34	9.9	37948 2	AF079138
30	34	9.9	43280 2	SF078289
31	34	9.9	11353 54	AC011509
32	33.8	9.8	674 1	DVCYTC3
33	33.8	9.8	1310 7	OSAO11078
34	33.8	9.8	1384 7	OSAI8624
35	33.8	9.8	1393 7	TAEI8626
36	33.8	9.8	19630 1	SC3F9
37	33.8	9.8	50394 42	AC014393
38	33.6	9.7	34393 42	AC014983
39	33.6	9.7	79408 45	AC021683
40	33.4	9.7	1436 8	AF033540
41	33.4	9.7	33620 2	SC20
42	33.2	9.6	43147 1	SC4A10
43	33	9.6	1240 7	DUNCBP
44	33	9.6	1518 12	CP073590
45	33	9.6	2311 7	HVMAXR

ALIGNMENTS

AF123653 Homo sapi  
AF123654 Homo sapi  
AF123655 Homo sapi  
AF123656 Homo sapi  
AF123657 Homo sapi  
AF123658 Homo sapi  
AF123659 Homo sapi  
AF123652 Homo sapi  
PSEMPA  
E03105 DNA encodin  
E15909 gDNA encodi  
D31702 Sulfate-red  
AL031514 Streptomy  
AF050418 Mus muscu  
M24258 Maize amyl  
X03935 Zea mays wa  
AC011772 Homo sapi  
AF040746 Mus muscu  
M64551 Streptomyce  
AL021411 Streptomy  
U57845 Hordeum vul  
AC005802 Leishmani  
AC007860 Homo sapi  
AB014541 Homo sapi  
AC008755 Homo sapi  
AF159691 Myxococcu  
M77475 Hordeum vul  
L36817 Alcaligenes  
AF079138 Streptomy  
U78289 Streptomyce  
AC011509 Homo sapi  
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AJ011078 Oryza sat  
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Y18626 Trilicium ae  
AL023863 Streptomy  
AC014393 Drosophili  
AC014983 Drosophili  
AC021683 Homo sapi  
AF033540 Lolium pe  
AL136058 Streptomy  
AL109663 Streptomy  
M23531 D.salina ma  
U73590 Cavia porce  
X07932 Barley mRNA

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LOCUS Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.
DEFINITION AF123659
ACCESSION AF123659.1 GI:4572475
VERSION human.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 5492)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
MEDLINE 99199287
REFERENCE 2 (bases 1 to 5492)
AUTHORS Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2335 10th street, Philadelphia, PA 19107, USA
FEATURES
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LLKQOLKESQTEVNAKASEILGL
ENELQKKNKAEILLREKVNLEQ
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LARQDSAGEPLEVLEGADIPYI
BASE COUNT 1137 a 1704 c 1565 g 1
ORIGIN

Query Match 100.0%; Score 639; DB 40; Leu..
Best Local Similarity 100.0%; Pred. No. 1e-79;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaggtgaacgcgaagctagcgaatctgggtctcaagcacagctgaaggacacgcgg 60
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Qy 61 gdcagctggagggcctgagctgagcaccacagcagcctgagggcgccctgcgcaccaag 120
Db 1381 GCGAAGCTGGAGGGCCTGGAGCTGAGACCCAGGACCTGGAGGGCGCCCTGCCGCCAAG 1440
Qy 121 ggcctgagctggagggctgtgagaatgagctgcagcgcaagaagacgagcgagctg 180
Db 1441 GGCCTGAGCTGGAGGCTGTGTGAGAAATGAGCTGCAGCGCAAGAAAGACGAGCGGAGCTG 1500
Qy 181 ctgcgggagaggtgagctgctgctgagcagagagctgagagagctgagggcccgccgccc 240
Db 1501 CTCGGGAGAGGUGAACCCTGCTGGAGCAGAGAGCTGCAGGAGCTGCGGGGCCAGCGCC 1560

123659
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Gencore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2000, 02:09:08 ; Search time 1236.72 Seconds  
(without alignments)  
-271.374 Million cell updates/sec

Title: PCT-US00-04950-1\_COPY\_112\_456  
Perfect score: 345  
Sequence: 1 tcgcagtcacagctgcgca.....gcaggaagcaaatggg 345

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

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44: gb\_da44.\*

RECEIVED  
JAN 04 2001  
TECH CENTER 1600/2900

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	345	100.0	9108	40	AF123653	AF123653 Homo sapi
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4	286	82.9	1614	40	AF123656	AF123656 Homo sapi
5	286	82.9	1692	40	AF123657	AF123657 Homo sapi
6	286	82.9	1722	40	AF123658	AF123658 Homo sapi
7	286	82.9	5492	40	AF123659	AF123659 Homo sapi
8	106	30.7	231	40	AF123652	AF123652 Homo sapi
9	39.6	11.5	3496	1	PSEMPA	PSEMPA
10	39.6	11.5	3496	3	E03105	E03105 Pseudomonas
11	38.6	11.2	324	5	E15909	E15909 gDNA encod
12	38.6	11.2	873	1	DVUPCC3	D31702 Sulfate-red
13	36.8	10.7	25970	1	SC2H4	AL031514 Streptomy
14	36.6	10.6	1884	12	AF050418	AF050418 Mus muscu
15	36.4	10.6	4800	7	M2EMAX	M2458 Malze amylo
16	36.4	10.6	4800	7	ZNMWAX	X03935 Zea mays wa
17	35.6	10.3	151291	44	AC011772	AC011772 Homo sapi
18	35.2	10.2	2072	12	AF040746	AF040746 Mus muscu
19	35.2	10.2	4501	2	STXNLNA	M64551 Streptomyce
20	35.2	10.2	35654	1	SC7H1	AL021411 Streptomy
21	34.8	10.1	12339	8	HVU57845	U57845 Hordeum vul
22	34.8	10.1	29641	35	AC005802	AC005802 Leishman
23	34.6	10.1	186298	40	AC007860	AC007860 Homo sapi
24	34.6	10.0	5140	9	AB014541	AB014541 Homo sapi
25	34.6	10.0	190702	44	AC008755	AC008755 Homo sapi
26	34.4	10.0	3931	2	AF159691	AF159691 Myxococcu
27	34	9.9	4788	7	BLXSIDIA	M77475 Hordeum vul
28	34	9.9	9830	2	AFAGBD	L36817 Alcailligenes
29	34	9.9	37948	2	AF079138	AF079138 Streptomy
30	34	9.9	43280	2	SF078289	U78289 Streptomyce
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32	33.8	9.8	674	1	DVCYTC3	X04304 Desulfovibr
33	33.8	9.8	1310	7	OSAO11078	Y18624 Oryza sativ
34	33.8	9.8	1384	7	OSAO11078	Y18624 Oryza sativ
35	33.8	9.8	1393	7	TAE18626	Y18626 Trillium ae
36	33.8	9.8	19830	1	SC3F9	AL023862 Streptomy
37	33.8	9.8	50394	42	AC014393	AC014393 Drosophil
38	33.6	9.7	34393	42	AC014983	AC014983 Drosophil
39	33.6	9.7	79408	45	AC021683	AC021683 Homo sapi
40	33.4	9.7	1436	8	AF033540	AF033540 Lolium pe
41	33.4	9.7	33820	2	SCE20	AL136058 Streptomy
42	33.2	9.6	43147	7	SC4A10	AL109663 Streptomy
43	33	9.6	1240	7	DUNCBP	M23531 D. salina ma
44	33	9.6	1518	12	CPU73590	U73590 Cavia porce
45	33	9.6	2311	7	HVMAXYR	X07932 Barley mRNA

## ALIGNMENTS